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Fig. 9

Comparison of amino acid sequence of the "original" Pig-baboon chimeric uricase ("chimera") with that of "Baboon D3H" uricase (Baboon except for His replacing Asp at amino acid 3)

Pig uricase:

Pig cDNA from 1 to 915 (end)

"Baboon D3H" uricase:

"Baboon D3H" cDNA from 1 to 915 (end)

[GCG GAP program]

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 1493 Length: 305
Ratio: 4.895 Gaps: 0
Percent Similarity: 94.098 Percent Identity: 90.820

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

Pig.pep x baboon D3H.pep

June 25, 1998 17:44 ..

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Pig   1 MAHYRNDYKKNDEVEFVRTGYGKDMIKVLHIQRDGKYHSIKEVATSVQLT 50
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
Bab   1 MAHYHNNYKKNDELEFVRTGYGKDMVKVLHIQRDGKYHSIKEVATSVQLT 50
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.

51  LSSKKDYLGHDNSDVIPTDTIKNTVNVLAKFKGIKSIETFAVTICEHFLS 100
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
51  LSSKKDYLGHDNSDIPTDTIKNTVHVLAKFKGIKSIETAFGVNICEYFLS 100
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.

101  SFKHVIRAQVYVEEVPWKRFEKNGVKHVFHAFIYTPTGTHFCEVEQIRNGP 150
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
101  SFNHVIRAQVYVEEIPWKRLEKNGVKHVFHAFIHTPTGTHFCEVEQLRSGP 150
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.

151  PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH 200
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
151  PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH 200
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.

201  QGRDVFDEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLYDIQVLTGQV 250
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
201  QCRDVFDEATWGTIRDVLVLEKFAGPYDKGEYSPSVQKTLYDIQVLSLSRV 250
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.

251  PEIEDMEISLPNIHYLNIDMSKMGLINKEEVLLPLDNPYGRITGTVKRKL 300
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
251  PEIEDMEISLPNIHYFNIDMSKMGLINKEEVLLPLDNPYKITGTVKRKL 300
      |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.

301  TSRL* 305
      .|||||
301  SSRL* 305

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Fig. 10

Comparison of amino acid sequence of the "original" Pig-baboon chimeric uricase ("chimera") with that of "Baboon D3H" uricase (Baboon except for His replacing Asp at amino acid 3)

"Chimera" uricase:

Pig cDNA from 1 to 674 (Apa site) and then Baboon cDNA from 675 to 915 (end)

"Baboon D3H" uricase:

"Baboon D3H" cDNA from 1 to 915 (end)

[GCG GAP program]

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 1516 Length: 305
Ratio: 4.970 Gaps: 0
Percent Similarity: 95.738 Percent Identity: 92.787

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

chimera.pep x baboon D3H.pep June 25, 1998 17:18 ..

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chim  1 MAHYRNDYKKNDEVEFVRTGYGKDMIKVLHIQRDGKYHSIKEVATSVQLT 50
      ||||| |.| |||||. ||||| ||||| : ||||| ||||| ||||| ||||| |||||
Bab   1 MAHYHNNYKKNDELEFVRTGYGKDMVKVLHIQRDGKYHSIKEVATSVQLT 50
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

51  LSSKKDYLHGDNSDVIPTDTIKNTVNVLAKFKGIKSIETFAVTICEHFLS 100
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51  LSSKKDYLHGDNSDIIPTDTIKNTVHVLAKEFKGIKSIETAFGVNICEYFLS 100
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

101 SFKHVIRAQVYVEEVPWKRFEKNGVKVHAFIYTPTGTHFCEVEQIRNGP 150
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
101 SFNHVIRAQVYVEEIPWKRLEKNGVKVHAFIHTPTGTHFCEVEQLRSGP 150
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

151 PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH 200
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
151 PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH 200
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

201 QGRDVFDEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLYDIQVLSLSRV 250
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
201 QCRDVFDEATWGTIRDLVLEKFAGPYDKGEYSPSVQKTLYDIQVLSLSRV 250
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

251 PEIEDMEISLPNIHYFNIDMSKMGLINKEEVLLPLDNPYGKITGTGTVKRKL 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
251 PEIEDMEISLPNIHYFNIDMSKMGLINKEEVLLPLDNPYGKITGTGTVKRKL 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

301 SSRL* 305
      |||||
301 SSRL* 305

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Fig. 11-1

Bestfit (GCG software) comparison of coding sequences of the cDNAs of Pig KS uricase ("PKS") vs. pig uricase

"Pig KS" uricase:

Pig cDNA from 1 to 864 (NdeI site) and then Baboon 865 to 915 (end)

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: -9.000

Quality: 9036 Length: 915
Ratio: 9.875 Gaps: 0
Percent Similarity: 99.344 Percent Identity: 99.344

Match display thresholds for the alignment(s):

| = IDENTITY
: = 5
. = 1

pigKS.seq x pig.seq July 25, 1998 10:14 ..

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PKS   1 ATGGCTCATTACCGTAATGACTACAAAAAGAATGATGAGGTAGAGTTTGT 50
      |||||||
pig   1 ATGGCTCATTACCGTAATGACTACAAAAAGAATGATGAGGTAGAGTTTGT 50

      51 CCGAACTGGCTATGGGAAGGATATGATAAAAGTTCTCCATATTCAGCGAG 100
      |||||||
      51 CCGAACTGGCTATGGGAAGGATATGATAAAAGTTCTCCATATTCAGCGAG 100

      101 ATGGAAAATATCACAGCATTAAAGAGGTGGCAACTTCAGTGCAACTGACT 150
      |||||||
      101 ATGGAAAATATCACAGCATTAAAGAGGTGGCAACTTCAGTGCAACTGACT 150

      151 TTGAGCTCCAAAAAAGATTACCTGCATGGAGACAATTCAGATGTCATCCC 200
      |||||||
      151 TTGAGCTCCAAAAAAGATTACCTGCATGGAGACAATTCAGATGTCATCCC 200

      201 TACAGACACCATCAAGAACACAGTTAATGTCCTGGCGAAGTTCAAAGGCA 250
      |||||||
      201 TACAGACACCATCAAGAACACAGTTAATGTCCTGGCGAAGTTCAAAGGCA 250

      251 TCAAAAGCATAGAACTTTTGCTGTGACTATCTGTGAGCATTCCTTTTCT 300
      |||||||
      251 TCAAAAGCATAGAACTTTTGCTGTGACTATCTGTGAGCATTCCTTTTCT 300

      301 TCCTTCAAGCATGTCATCAGAGCTCAAGTCTATGTGGAAGAAGTTCCTTG 350
      |||||||
      301 TCCTTCAAGCATGTCATCAGAGCTCAAGTCTATGTGGAAGAAGTTCCTTG 350

      351 GAAGCGTTTTTGAAAAGAATGGAGTTAAGCATGTCCATGCATTTATTTATA 400
      |||||||
      351 GAAGCGTTTTTGAAAAGAATGGAGTTAAGCATGTCCATGCATTTATTTATA 400
  
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